

32. (New) The method of claim 22, wherein the phytyl/prenyltransferase polynucleotide comprises a member selected from the group consisting of:

- (a) a polynucleotide that encodes a polypeptide of SEQ ID Nos.: 4, 12, 14, 16, 18, 20, 22, 24, 26 or 28;
- (b) a polynucleotide comprising the sequence set forth in SEQ ID Nos.: 3, 11, 13, 15, 17, 19, 21, 23, 25, 27 or 29; and
- (c) a polynucleotide complementary to a polynucleotide of (a) or (b).

83. (New) The method of claim 22, wherein the phytyl/prenyltransferase polynucleotide comprises a polynucleotide which selectively hybridizes, under stringent hybridization conditions and a wash in 2X SSC at 50°C, to a hybridization probe the polynucleotide sequence of which consists of the coding sequence of SEQ ID Nos.: 3, 11, 13, 15, 17, 19, 21, 23, 25 or 27, or the complement of the coding sequence of SEQ ID Nos.: 3, 11, 13, 15, 17, 19, 21, 23, 25 or 27.

34. (New) The method of claim 27, wherein the phytyl/prenyltransferase polynucleotide comprises a member selected from the group consisting of:

- (a) a polynucleotide having at least 70% sequence identity to the entire coding sequence of SEQ. ID Nos.: 1, 3, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27 or 29, wherein the % sequence identity is determined by GAP using default parameters, and
- (b) a polynucleotide complimentary to a polynucleotide of (a).

35. (New) The method of claim 27, wherein the phytyl/prenyltransferase polynucleotide comprises a member selected from the group consisting of:

- (a) a polynucleotide that encodes a polypeptide of SEQ ID Nos.: 4, 12, 14, 16, 18, 20, 22, 24, 26 or 28;
- (b) a polynucleotide comprising the sequence set forth in SEQ ID Nos.: 3, 11, 13, 15, 17, 19, 21, 23, 25, 27 or 29; and
- (c) a polynucleotide complementary to a polynucleotide of (a) or (b).

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36. (New) The method of claim 27, wherein the phytyl/prenyltransferase polynucleotide comprises a polynucleotide which selectively hybridizes, under stringent hybridization conditions and a wash in 2X SSC at 50°C, to a hybridization probe the polynucleotide sequence of which consists of the coding sequence of SEQ ID Nos.: 3, 11, 13, 15, 17, 19, 21, 23, 25 or 27, or the complement of the coding sequence of SEQ ID Nos.: 3, 11, 13, 15, 17, 19, 21, 23, 25 or 27.
37. (New) The method of claim 29, wherein the phytyl/prenyltransferase polynucleotide comprises a member selected from the group consisting of:
- (a) a polynucleotide having at least 70% sequence identity to the entire coding sequence of SEQ. ID Nos.: 1, 3, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27 or 29, wherein the % sequence identity is determined by GAP using default parameters, and
  - (b) a polynucleotide complementary to a polynucleotide of (a).
38. (New) The method of claim 29 wherein the phytyl/prenyltransferase polynucleotide comprises a member selected from the group consisting of:
- (a) a polynucleotide that encodes a polypeptide of SEQ ID Nos.: 4, 12, 14, 16, 18, 20, 22, 24, 26 or 28;
  - (b) a polynucleotide comprising the sequence set forth in SEQ ID Nos.: 3, 11, 13, 15, 17, 19, 21, 23, 25, 27 or 29; and
  - (c) a polynucleotide complementary to a polynucleotide of (a) or (b).
39. (New) The method of claim 29, wherein the phytyl/prenyltransferase polynucleotide comprises a polynucleotide which selectively hybridizes, under stringent hybridization conditions and a wash in 2X SSC at 50°C, to a hybridization probe the polynucleotide sequence of which consists of the coding sequence of SEQ ID Nos.: 3, 11, 13, 15, 17, 19, 21, 23, 25 or 27, or the complement of the coding sequence of SEQ ID Nos.: 3, 11, 13, 15, 17, 19, 21, 23, 25 or 27.
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